GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 03:44:44 ; Search time 288 Seconds
(without alignments)
117.292 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	21	AAZ90403	Phosphorothioated
	2	15	100.0	19	22	AAF98894	Immunostimulatory
	3	15	100.0	19	24	ABL38703	Immunostimulatory
c	4	15	100.0	24	14	AAQ52043	Breast cancer spec
c	5	15	100.0	70	20	AAX80767	Promoter region of
	6	14	93.3	15	19	AAV40434	US-1 antisense oli
	7	14	93.3	51	22	AAI75566	Human silent SNP c
c	8	13.4	89.3	24	19	AAV22685	PCR primer HN40 us
c	9	13.4	89.3	29	22	AAS09199	PCR primer #1 used
	10	13	86.7	14	16	AAQ92762	c-erbB-2 antisense
	11	13	86.7	16	19	AAV48736	ErbB-2 gene antise
c	12	13	86.7	19	21	AAA53776	Forward primer for
c	13	13	86.7	19	22	AAD15845	Human HER-2 ECD co
c	14	13	86.7	19	24	AAD32531	HER-2 extracellula
	15	13	86.7	20	20	AAV84090	PCR primer MTL(P)
c	16	13	86.7	20	22	AAS00677	Human consensus se
	17	13	86.7	20	22	AAF26607	Maize metallothion
	18	12.4	82.7	20	21	AAA74062	Reverse PCR primer
c	19	12.4	82.7	22	20	AAV08115	Primer Vbeta5 for
c	20	12.4	82.7	24	24	ABN83663	Gamma-glutamylcyst
	21	12.4	82.7	47	20	AAZ01091	Probe for human PG
c	22	12.4	82.7	50	22	AAI77430	Human silent SNP c
	23	12.4	82.7	51	22	AAI75567	Human silent SNP c
c	24	12.4	82.7	51	22	AAI77426	Human silent SNP c
c	25	12.4	82.7	51	22	AAI77427	Human silent SNP c
c	26	12.4	82.7	51	22	AAI77428	Human silent SNP c
	27	12.4	82.7	60	24	ABN33270	Human spliced tran
c	28	12.4	82.7	65	24	ABN54380	Mouse spliced tran
	29	12.4	82.7	98	24	ABN60554	Human cancer relat
c	30	12	80.0	22	19	AAV17078	Oligonucleotide 6
c	31	12	80.0	27	19	AAV36673	Nucleotide sequenc
c	32	12	80.0	53	19	AAV36662	Nucleotide sequenc
	33	12	80.0	60	24	ABN48619	Human spliced tran
c	34	12	80.0	62	19	AAV36663	Nucleotide sequenc
	35	12	80.0	65	24	ABN54104	Mouse spliced tran
	36	12	80.0	65	24	ABN54738	Mouse spliced tran
	37	12	80.0	97	19	AAV17076	Oligonucleotide 4
c	38	11.8	78.7	19	24	AAD32361	Human LSG 414885 e
	39	11.8	78.7	20	21	AAA12081	Human ICAM-1 antis
	40	11.8	78.7	20	24	ABL45607	Human chromosome 2
c	41	11.8	78.7	22	21	AAA52945	Mouse EphA4 gene P
	42	11.8	78.7	28	21	ABK12010	Thrombopoietin rel
	43	11.8	78.7	32	21	AAA52982	HCV-1a E2 forward
	44	11.8	78.7	33	24	ABL55542	Haploid sperm cell
c	45	11.8	78.7	42	21	AAA12095	Human ICAM-1 DNA f

ALIGNMENTS

RESULT 1
AAZ90403
ID AAZ90403 standard; DNA; 15 BP.
XX
AC AAZ90403;
XX
DT 30-MAY-2000 (first entry)
XX
DE Phosphorothioated ASO directed against HER-2 gene.
XX
KW Radiation; drug resistance; HER-2; raf-1; radioresistant; tumour;
KW cancer; restenosis; osteoarthritis; neurological; pre-eclampsia;
KW intestinal abnormality; antisense; ss.
XX
OS Homo sapiens.
XX
PN US6027892-A.
XX
PD 22-FEB-2000.
XX
PF 16-DEC-1997; 97US-0991830.
XX
PR 30-DEC-1996; 96US-0034160.
XX
PA (CHAN/) CHANG E H.
PA (PIRO/) PIROLLO K F.
XX
PI Chang EH, Pirollo KF;
XX
DR WPI; 2000-194828/17.
XX
PT Reducing radiation or drug resistance in a cell comprises introduction

Double Pat??

PT of antisense nucleic acid for treating or diagnosing cancer,
PT restenosis, osteoarthritis, neurological and intestinal abnormalities
PT and pre-eclampsia -
XX
PS Claim 4; Column 9; 18pp; English.
XX
CC The invention provides a method for reducing radiation or drug resistance
CC of a cell, in vitro, which does not overexpress HER-2 or raf-1 genes.
CC The method comprises introducing to the cell an antisense nucleic acid
CC comprising a segment complementary to HER-2 or raf-1. The method is
CC useful for increasing drug and radiation sensitivity in a cell,
CC particularly in the treatment of radioresistant tumours. The antisense
CC nucleic acids are useful for treating or diagnosing cancer, restenosis,
CC osteoarthritis, neurological and intestinal abnormalities and
CC pre-eclampsia. The present sequence represents a phosphorothioated
CC antisense oligo (ASO) directed against HER-2 gene.
XX
SQ Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 15; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCACT 15
||||||||||||||||
Db 1 TCCATGGTGCTCACT 15

RESULT 2
AAF98894
ID AAF98894 standard; DNA; 19 BP.
XX
AC AAF98894;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #10.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US26383.
XX
PR 25-SEP-1999; 99US-0156113.
PR 27-SEP-1999; 99US-0156135.
PR 23-AUG-2000; 2000US-0227436.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
XX
PS Disclosure; Page 38; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCACT 15
||||||||||||||||
Db 4 TCCATGGTGCTCACT 18

RESULT 3
ABL38703
ID ABL38703 standard; DNA; 19 BP.
XX
AC ABL38703;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 66.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US20154.
XX
PR 22-JUN-2000; 2000US-213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer -
XX
PS Disclosure; Page 111; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in
CC the exemplification of the invention.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 19;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCACT 15
||||||||||||||||
Db 4 TCCATGGTGCTCACT 18

RESULT 4
AAQ52043/c
ID AAQ52043 standard; RNA; 24 BP.
XX
AC AAQ52043;
XX
DT 26-MAY-1994 (first entry)
XX
DE Breast cancer specific mRNA ribozyme cleavable nucleotide (159).
XX
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
OS Homo sapiens.
XX
PN WO9323057-A.
XX
PD 25-NOV-1993.
XX
PF 13-MAY-1993; 93WO-US04573.
XX
PR 14-MAY-1992; 92US-0882822.
PR 14-MAY-1992; 92US-0882885.
PR 26-AUG-1992; 92US-0936110.
PR 26-AUG-1992; 92US-0936421.
PR 26-AUG-1992; 92US-0936422.
PR 26-AUG-1992; 92US-0936531.
PR 26-AUG-1992; 92US-0936532.
PR 07-DEC-1992; 92US-0987131.
PR 19-JAN-1993; 93US-0006122.
PR 19-JAN-1993; 93US-0008910.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Thompson JD;
XX
DR WPI; 1993-386203/48.
XX
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT associated with tumours or mRNA expressed from gene encoding
PT multiple drug resistance
XX
PS Claim 3; Fig 8; 69pp; English.
XX
CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC and lung cancer. The full length mRNAs containing these target
CC sequences, encode aberant cellular proteins which are able to control
CC cellular proliferation and are directly linked to a leukemic
CC phenotype. These target sequences are identified by the ribozyme of
CC the invention. The ribozymes is formed in a hammerhead motif, but may
CC also be formed in the motif of a hairpin, hepatitis delta virus, group
CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
CC the development or expression of a transformed phenotype in man and
CC other animals by modulating expression of the corresponding gene.
CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC cells elicits inhibition of the transformed state. Multiple drug
CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC drug resistance used by transformed cells and thus enhances drug
CC therapies for tumours. The ribozymes may also be used to study
CC genetic drift and mutations within cells.
XX
SQ Sequence 24 BP; 6 A; 7 C; 8 G; 3 U; 0 other;

Query Match 100.0%; Score 15; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCACT 15
||||||||||||||||
Db 21 TCCATGGTGCTCACT 7

RESULT 5
AAX80767/c
ID AAX80767 standard; DNA; 70 BP.
XX
AC AAX80767;
XX
DT 26-OCT-1999 (first entry)
XX
DE Promoter region of HER-2 DNA target sequence.
XX
KW HER-2; c-erb-B2; target sequence; antisense molecule; HERMYC1; HERMYC2;
KW HERMYC1R; HERMYC2R; breast cancer; c-myc; promoter region; HER 5';
KW topological linkage; padlock DNA; malignancy; metastasis; tumour;
KW transcription factors; gene therapy; cultured cell; amplification;
KW antisense technology; therapeutic modulation; ss.
XX
OS Homo sapiens
XX
FH Key Location/Qualifiers
FT misc_binding 6..20
FT /*tag= a
FT /bound_moiety= "HERMYC1 or HERMYC1R antisense molecule"
FT /note= "Forms a duplex in the presence of HERMYC1 in
FT AAX80768 or HERMYC1R antisense molecule in AAX80770"
FT misc_binding 37..50
FT /*tag= b
FT /bound_moiety= "HERMYC2 or HERMYC2R antisense molecule"
FT /note= "Forms a duplex in the presence of HERMYC2 in
FT AAX80769 or HERMYC2R antisense molecule in AAX80771"
XX
PN WO9909045-A1.
XX
PD 25-FEB-1999.
XX
PF 20-AUG-1998; 98WO-US17268.
XX
PR 20-AUG-1997; 97US-0056742.
XX
PA (SOMA-) SOMAGENICS INC.
XX
PI Johnston BH, Kazakov SA, Kisich KO;
XX
DR WPI; 1999-228889/19.
XX
PT A new antisense molecule which topologically links to target mRNA
XX
PS Example 5; Fig 8; 134pp; English.
XX
CC The present sequence is the 5'promoter region of HER-2 oncogene, that

CC undergoes genetic alterations along with c-myc gene and is associated
CC with aggressive breast cancer and poor prognosis. Overexpression of
CC HER-2 gene has been shown to enhance malignancy and metastasis.
CC Repression of HER-2 in mouse tumours leads to suppression of tumour
CC growth and longer life of the animal. This can be done by using padlock
CC DNAs, HERMYC1, HERMYC1R, HERMYC2 and HERMYC2R, that target a G rich
CC sequence in the promoter region. It inhibits binding of transcription
CC factors. This sequence can be used as a target sequence in antisense
CC technology for therapeutic modulation of gene expression in cultured
CC cells and whole animals, for gene function analysis and target
CC validation for gene therapy and for the detection and amplification of
CC nucleic acids.
XX
SQ Sequence 70 BP; 6 A; 25 C; 26 G; 13 T; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 70;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCACT 15
||||||||||||||||
Db 28 TCCATGGTGCTCACT 14

promoter region

RESULT 6
AAV40434
ID AAV40434 standard; DNA; 15 BP.
XX
AC AAV40434;
XX
DT 28-SEP-1998 (first entry)
XX
DE US-1 antisense oligonucleotide used to down regulate ERBB2 oncogene.
XX
KW Antisense oligonucleotide; down regulate; erbB-2; oncogene;
KW tyrosine kinase; breast cancer; radioisotope; hybridisation; probe;
KW US-1; US-3; US-4; US-5; UT-1; US-D; SC-3; TRACER; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9820168-A1.
XX
PD 14-MAY-1998.
XX
PF 03-NOV-1997; 97WO-US20910.
XX
PR 04-NOV-1996; 96US-0740821.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Inglehart JD, Marks JR, Vaughn JP;
XX
DR WPI; 1998-286977/25.
XX
PT Antisense oligonucleotides that down regulate the erbB-2 oncogene -
PT useful to inhibit ERBB2 tyrosine kinase receptor expression in
PT cancer cells to treat epithelial cell, breast, ovarian, lung or
PT colon cancer
XX
PS Example 6; Page 15; 31pp; English.
XX
CC The antisense oligonucleotides AAV40432-V40439 were used to down
CC regulate the erbB-2 oncogene. This oncogene codes for a 185kD tyrosine
CC kinase linked transmembrane protein which in 30-50% of primary breast
CC cancers is overexpressed. The oligonucleotides are able to inhibit the
CC overexpression of ERBB2 tyrosine kinase receptor in a cell, which can be
CC done by targeting the antisense oligonucleotides to the erbB-2 oncogene.
CC By labelling the oligonucleotides with, for example, a radioisotope,
CC they can also be used as hybridisation probes to detect the ERBB2 gene.
CC The oligonucleotides were designated the following names, followed by
CC the location in the erbB-2 gene that they target: US-1 (166-180); US-3
CC (160-174); US-4 (173-187); US-5 (178-192); UT-1 (151-165); US-D
CC (US-1 scrambled control); SC-3 (US-3 scrambled control); TRACER
CC (fluoresceinated tracer). It was found that all of the oligonucleotides
CC (apart from the controls) inhibited the erbB-2 protein, however with
CC varying degrees of effectiveness. US-3 and UT-1 were identified as
CC being the most efficient oligonucleotides at inhibiting erbB-2. The
CC oligonucleotides are useful in vivo to treat cancer (especially
CC epithelial cell, breast, ovarian, lung or colon cancer) in a human or
CC other animal, especially when the cancer is characterised by cells that
CC overexpress the ERBB2 tyrosine kinase receptor.
XX
SQ Sequence 15 BP; 2 A; 6 C; 3 G; 4 T; 0 other;

Query Match 93.3%; Score 14; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCAC 14
||||||||||||||
Db 2 TCCATGGTGCTCAC 15

RESULT 7
AAI75566
ID AAI75566 standard; DNA; 51 BP.
XX
AC AAI75566;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2507.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 818; 2653pp; English.
XX
CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The

```
CC   antibodies may also be used to down regulate expression and activity.
CC   The antibodies may also be used as diagnostic agents for detecting the
CC   presence of polymorphic polypeptides in samples.
XX
SQ   Sequence 51 BP; 7 A; 14 C; 15 G; 15 T; 0 other;

  Query Match             93.3%;  Score 14;  DB 22;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 CCATGGTGCTCACT 15
          ||||||||||||||
Db     17 CCATGGTGCTCACT 30


RESULT 8
AAV22685/c
ID   AAV22685 standard; DNA; 24 BP.
XX
AC   AAV22685;
XX
DT   20-JUL-1998  (first entry)
XX
DE   PCR primer HN40 used to amplify ErbB-2.
XX
KW   ErbB-2 protein; vaccine; T-cell damage; activation; T-cell; treatment;
KW   prevention; viral disease; cancer; autoimmune disorder; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9809650-A1.
XX
PD   12-MAR-1998.
XX
PF   05-SEP-1997;   97WO-JP03123.
XX
PR   06-SEP-1996;   96JP-0236937.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
PI   Nakamura H,  Shiku H,  Sunamoto J;
XX
DR   WPI; 1998-193326/17.
XX
PT   Vaccine preparation comprises antigen and hydrophobic polysaccharide
PT    - e.g. mannan containing sterol groups for treating, e.g. cancer
XX
PS   Example 1; Page 9; 27pp; English.
XX
CC   PCR primers AAV22685-86 are used to amplify DNA encoding ErbB-2
CC   proteins. The specification describes a vaccine preparation that
CC   comprises an antigen and, optionally, a hydrophobic polysaccharide (HPS)
CC   optionally as a composite. The antigen is a protein, such as ErbB-2 class
CC   1-9 proteins, which initiate T-cell damage. The vaccine activates T-cells
CC   and is useful for the treatment and prevention of viral diseases, cancer
CC   and autoimmune disorders.
XX
SQ   Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;

  Query Match             89.3%;  Score 13.4;  DB 19;  Length 24;
  Best Local Similarity   93.3%;  Pred. No. 5.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCACT 15
          ||||||||| |||||
Db     21 TCCATGGTGATCACT 7


RESULT 9
AAS09199/c
ID   AAS09199 standard; DNA; 29 BP.
XX
AC   AAS09199;
XX
DT   07-NOV-2001  (first entry)
XX
DE   PCR primer #1 used to amplify cDNA encoding murine CCR7.
XX
KW   Cell fusion assay; fluorescence resonance energy transfer; FRET;
KW   beta-lactamase; inhibition of cell fusion; CD4; cytokine receptor;
KW   viral disease; HIV-1 infection; mouse; murine; CCR7; Th1 cell;
KW   PCR primer; ss.
XX
OS   Mus sp.
XX
PN   WO200160995-A1.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04677.
XX
PR   17-FEB-2000; 2000US-0183309.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Sullivan KA,  Benincasa D,  Cascieri MA,  Mitnaul LJ,  Shiao L;
PI   Tota MR;
XX
DR   WPI; 2001-536569/59.
XX
PT   Determining the amount of fusion that occur between two cells comprises
PT   measurement of fluorescence energy transfer -
XX
PS   Disclosure; Page 14; 59pp; English.
XX
CC   The present invention relates to a method for determining the amount
CC   of fusion that occurs between two cells, one of which contains the
CC   enzyme beta-lactamase and the other of which contains a fluorescent
CC   substrate of beta-lactamase. The method comprises the measurement of
CC   fluorescence resonance energy transfer (FRET). The invention also
CC   provides methods of identifying inhibitors of the fusion of two
CC   types of cells, particularly when fusion is mediated by the
CC   interaction of a viral protein and target cellular proteins e.g. CD4
CC   and cytokine receptors. The methods are useful for identifying
CC   substances that are useful for the treatment of viral diseases,
CC   particularly for the identification of inhibitors of HIV-1 infection.
CC   The present sequence for PCR primer #1 is used with PCR primer #2
CC   (AAS09200) to amplify cDNA encoding CCR7 from murine Th1 cells.
XX
SQ   Sequence 29 BP; 9 A; 8 C; 10 G; 2 T; 0 other;

  Query Match             89.3%;  Score 13.4;  DB 22;  Length 29;
  Best Local Similarity   93.3%;  Pred. No. 6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCACT 15
          ||||||||||||| ||
Db     23 TCCATGGTGCTCTCT 9


RESULT 10
AAQ92762
ID   AAQ92762 standard; DNA; 14 BP.
XX
AC   AAQ92762;
XX
DT   13-FEB-1996  (first entry)
XX
DE   c-erbB-2 antisense nucleic acid #105.
XX
KW   Antisense nucleic acid; c-erbB-2; inhibition; fibroblast; neoplasm;
KW   p185-erbB-2 protein tyrosine kinase; tumour; breast cancer; detection;
KW   immune disease; angiogenesis; ss.
XX
OS   Synthetic.
XX
```

PN WO9517507-A1.
XX
PD 29-JUN-1995.
XX
PF 09-DEC-1994; 94WO-EP04094.
XX
PR 23-DEC-1993; 93EP-0120710.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Brysch W, Schlingensiepen G, Schlingensiepen K, Schlingensiepen R;
XX
DR WPI; 1995-240669/31.
XX
PT New anti:sense nucleic acid against C-erbB-2 - for treating or
PT preventing neoplasms, immune disease and angiogenesis, also for
PT diagnosis
XX
PS Claim 1; Page 48; 55pp; English.
XX
CC The sequences given in AAQ92658-762 are antisense nucleic acids which
CC hybridise with part of the mRNA and/or DNA encoding c-erbB-2. These
CC antisense nucleic acids are able to inhibit the expression of the
CC p185-erbB-2 protein tyrosine kinase activity and cell growth in a
CC number of tumour cells including breast cancer cells. Untransformed
CC normal fibroblasts are not growth inhibited by anti-c-erbB-2
CC antisense compounds suggesting that p185-erbB-2 plays a pathogenic
CC role in the growth of the above mentioned tumours. These antisense
CC oligonucleotides may be used in the prevention and treatment of
CC neoplasms, immune diseases and/or diseases involving pathological
CC angiogenesis when associated with c-erbB-2 expression. They may also
CC be used to detect expression of the relevant genes.
XX
SQ Sequence 14 BP; 2 A; 4 C; 4 G; 4 T; 0 other;

Query Match 86.7%; Score 13; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CATGGTGCTCACT 15
||||||||||||
Db 1 CATGGTGCTCACT 13

RESULT 11
AAV48736
ID AAV48736 standard; DNA; 16 BP.
XX
AC AAV48736;
XX
DT 15-OCT-1998 (first entry)
XX
DE ErbB-2 gene antisense oligonucleotide ErbB-2-28.
XX
KW ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-0101531.
XX
PR 31-JAN-1997; 97EP-0101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Brysch W, Schlingensiepen K;
XX
DR WPI; 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of
PT residues able to form two or three hydrogen bonds, have greater
PT activity and reduced toxicity, used therapeutically or to modulate
PT growth of cells in culture
XX
PS Claim 10; Fig 6a; 286pp; English.
XX
CC AAV48709-886 represent antisense oligonucleotides directed against the
CC ErbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted
CC in significant redcution in ErbB-2 protein expression, while
CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in
CC cases of cancer or (targeting TGF) for stimulating the immune system.
XX
SQ Sequence 16 BP; 2 A; 5 C; 5 G; 4 T; 0 other;

Query Match 86.7%; Score 13; DB 19; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CATGGTGCTCACT 15
||||||||||||
Db 1 CATGGTGCTCACT 13

RESULT 12
AAA53776/c
ID AAA53776 standard; DNA; 19 BP.
XX
AC AAA53776;
XX
DT 04-DEC-2000 (first entry)
XX
DE Forward primer for HER-2 extracellular domain cDNA.
XX
KW HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion;
KW extracellular domain IIIa; antagonist; intron 8; C-terminal extension;
KW truncated HER-2; p68; dimerization inhibitor; cytostatic; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200044403-A1.
XX
PD 03-AUG-2000.
XX
PF 20-JAN-2000; 2000WO-US01484.
XX
PR 20-JAN-1999; 99US-0234208.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Doherty JK, Clinton GM, Adelman JP;
XX
DR WPI; 2000-499287/44.
XX
PT Using polypeptides and antibodies that bind to the extracellular domain
PT of the receptor-like tyrosine kinase HER-2 to treat solid tumors of the
PT breast, lung, ovaries and colon
XX

PS Example 1; Page 14; 46pp; English.
XX
CC This primer, corresponding to HER-2 cDNA nucleotides 142-161, was used
CC to amplify the HER-2 extracellular domain. The reverse primers used are
CC shown in AAA53777 and AAA53778.
CC HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. The
CC extracellular domain of p185-HER-2 is proteolytically shed from breast
CC carcinoma cells in culture and is found in serum of some cancer patients
CC and may be a serum marker of metastatic breast cancer. An alternative
CC HER-2 mRNA of 4.8 kb with a 274 bp insert (intron 8) has been
CC identified. The retained intron is in-frame and encodes a 79 amino acid
CC extension designated ECDIIIa (the present sequence), which is inserted at
CC residue 340 of p185-HER-2. The alternative mRNA predicts a truncated
CC HER-2 protein (approximately 68 kDa) that lacks the transmembrane and
CC intracellular domains (see AAY97240). p68HER-2 specifically binds to
CC p185-HER-2 without activating HER-2. It could therefore block
CC dimerization of p185-HER-2. The p68HER-2 polypeptide binds to a site on
CC the ECD of HER-2 that is different from the site of binding for
CC Herceptin (RTM) (a marketed humanized monoclonal antibody that is used
CC for the treatment of cancer and binds to the ECD of HER-2). The methods,
CC compositions, polypeptides and antibodies are used to treat solid
CC tumours such as breast cancer, small cell lung carcinoma, ovarian cancer
CC and/or colon cancer, especially where over-expression of HER-2 is
CC indicated.
XX
SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 other;

Query Match 86.7%; Score 13; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCA 13
||||||||||||| |
Db 13 TCCATGGTGCTCA 1

RESULT 13
AAD15845/c
ID AAD15845 standard; DNA; 19 BP.
XX
AC AAD15845;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human HER-2 ECD coding sequence amplifying forward PCR primer #1.
XX
KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; PCR primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200161356-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US05327.
XX
PR 16-FEB-2000; 2000US-0506079.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Clinton G, Henner WD, Evans A;
XX
DR WPI; 2001-529934/58.
XX
PT New polypeptide, which binds to the extracellular domain of HER-2 for
PT the treatment of hard tumors -
XX
PS Example 1; Page 22; 61pp; English.
XX
CC The invention relates to novel HER-2 (herstatin-2) antagonist
CC particularly a polypeptide that binds to the extracellular domain (ECD)
CC of HER-2 at a site that is different from the binding site of humanised
CC antibody, Herceptin, at an affinity of at least 10^8. The present
CC invention is based upon the initial discovery of an alternative HER-2
CC mRNA transcript with 274 bp insert of intron 8. The translation product
CC of the alternative transcript is a truncated HER-2 protein designated
CC p68HER-2 which lacks the transmembrane and intracellular domains of
CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa.
CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
CC nucleic acids encoding these are useful to treat, diagnose and identify
CC solid tumours. The present sequence is a PCR primer used for amplifying
CC human HER2 ECD coding sequence.
XX
SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 other;

Query Match 86.7%; Score 13; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCA 13
||||||||||||| |
Db 13 TCCATGGTGCTCA 1

RESULT 14
AAD32531/c
ID AAD32531 standard; DNA; 19 BP.
XX
AC AAD32531;
XX
DT 18-JUN-2002 (first entry)
XX
DE HER-2 extracellular domain cDNA amplifying forward PCR primer A.
XX
KW Endothelial growth factor receptor; EGFR; cytostatic; tumour; herstatin;
KW HER-2 receptor tyrosine kinase; squamous cell carcinoma; lung; colon;
KW glial cell tumour; cell growth; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200214470-A2.
XX
PD 21-FEB-2002.
XX
PF 14-AUG-2001; 2001WO-US25502.
XX
PR 14-AUG-2000; 2000US-0638834.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Clinton GM;
XX
DR WPI; 2002-269185/31.
XX
PT Treating solid tumor characterized by expression of endothelial growth
PT factor receptor, involves administering recombinant herstatin that
PT binds to extracellular domain of the endothelial growth factor receptor
PT -
XX
PS Example 1; Page 29; 82pp; English.
XX
CC The present invention relates to a method for treating a solid tumour
CC characterised by endothelial growth factor receptor (EGFR) expression.
CC The method involves administering an agent that binds to an extracellular
CC domain (ECD) of EGFR. The invention also relates to a naturally occurring
CC inhibitor of HER-2 receptor tyrosine kinase called herstatin. The co-
CC expression of herstatin with p185HER2 causes a striking reduction in cell
CC growth that corresponds with suppression of p185 autophosphorylation. The
CC method or a pharmaceutical composition is useful for treating a solid
CC tumour (selected from squamous cell carcinoma, lung carcinoma, colon
CC carcinoma and glial cell tumour) characterised by EGFR expression. The
CC present sequence is a PCR primer used for amplifying HER-2 extracellular
CC domain cDNA.

```
XX
SQ   Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 other;

  Query Match             86.7%;  Score 13;  DB 24;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCA 13
          |||||||||||||
Db     13 TCCATGGTGCTCA 1


RESULT 15
AAV84090
ID   AAV84090 standard; DNA; 20 BP.
XX
AC   AAV84090;
XX
DT   12-MAR-1999  (first entry)
XX
DE   PCR primer MTL(P) used to amplify the iap, p35 and dad-1 genes.
XX
KW   Transgenic maize; Agrobacterium induced necrosis inhibition;
KW   metallothionein-like promoter; iap; p35; dad-1; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9854961-A2.
XX
PD   10-DEC-1998.
XX
PF   29-MAY-1998;   98WO-EP03215.
XX
PR   02-JUN-1997;   97US-0867869.
XX
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Hansen G;
XX
DR   WPI; 1999-059863/05.
XX
PT   Transforming plant cells using Agrobacterium - in conditions that
PT   inhibit Agrobacterium-induced necrosis
XX
PS   Example 8; Page 25; 47pp; English.
XX
CC   PCR primers AAV84090-93 were used for the amplification and detection
CC   of iap, p35 and dad-1 genes in transgenic maize callus, which was
CC   transformed with these genes using the method of the invention. The
CC   genes were cloned under the control of a metallothionein-like
CC   promoter (MLP). PCR primer AAV84090 hybridises promoter sequences, and
CC   is used in combination with each of the other primers in separate
CC   reactions. The specification describes a new method for transforming a
CC   plant cell with a gene of interest. The method comprises exposing the
CC   cell to Agrobacterium carrying that gene, under conditions which inhibit
CC   Agrobacterium induced necrosis (AIN). The method is used to transform
CC   plants with a gene of interest.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 other;

  Query Match             86.7%;  Score 13;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9.6e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCA 13
          |||||||||||||
Db      6 TCCATGGTGCTCA 18


Search completed: November 21, 2002, 05:08:27
Job time : 290 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 04:47:34 ; Search time 2148 Seconds
(without alignments)
113.097 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.4	89.3	75	13	BM023447	BM023447 ie80e10.y
	2	12.4	82.7	58	9	AI022662	AI022662 ox05h11.x
	3	12.4	82.7	74	9	AL362924	AL362924 AL362924
	4	12.4	82.7	77	14	W15664	W15664 mb52d02.r1
c	5	12.4	82.7	80	10	AV832470	AV832470 AV832470
	6	12.4	82.7	96	14	BQ566161	BQ566161 gi53e03.y
c	7	12	80.0	62	17	AZ648327	AZ648327 1M0517K13
	8	12	80.0	82	17	TA138D06P	AL465857 T. brucei
c	9	12	80.0	85	9	AI930840	AI930840 sb43a06.y
	10	12	80.0	90	9	AA690354	AA690354 vt31b01.r
c	11	12	80.0	92	17	AZ590927	AZ590927 1M0400G16
c	12	11.8	78.7	38	17	TA358F01P	AL494114 T. brucei
	13	11.8	78.7	65	9	AA285022	AA285022 zt25e10.s
	14	11.8	78.7	70	17	BH805669	BH805669 1008061H0
	15	11.8	78.7	72	17	AZ799758	AZ799758 2M0057G19
	16	11.8	78.7	80	17	BH895273	BH895273 3526_1_33
	17	11.8	78.7	86	17	BH806000	BH806000 1008063G0
c	18	11.8	78.7	89	13	BI472373	BI472373 fs02d01.y
	19	11.8	78.7	91	10	AV834264	AV834264 AV834264
	20	11.8	78.7	92	14	D18160	D18160 MUSGS00418
	21	11.8	78.7	97	14	T62112	T62112 yc66c02.r1
	22	11.8	78.7	99	17	AZ433742	AZ433742 1M0219H13
c	23	11.8	78.7	100	9	AA865812	AA865812 og97h05.s
c	24	11.4	76.0	22	17	AZ954618	AZ954618 2M0220E20
	25	11.4	76.0	41	9	AL799065	AL799065 AL799065
c	26	11.4	76.0	46	9	AA591686	AA591686 vl13g08.r
	27	11.4	76.0	50	9	AA108275	AA108275 EST0018 r
c	28	11.4	76.0	50	9	AU102591	AU102591 AU102591
c	29	11.4	76.0	50	9	AU102592	AU102592 AU102592
c	30	11.4	76.0	50	9	AU102593	AU102593 AU102593
c	31	11.4	76.0	50	9	AU102594	AU102594 AU102594
c	32	11.4	76.0	50	9	AU102595	AU102595 AU102595
c	33	11.4	76.0	50	9	AU107574	AU107574 AU107574
c	34	11.4	76.0	56	9	AI656187	AI656187 tt38f04.x
	35	11.4	76.0	60	17	AL752489	AL752489 Arabidops
	36	11.4	76.0	68	14	T72238	T72238 yc68d01.r1
c	37	11.4	76.0	73	9	AA220616	AA220616 my25f09.r
c	38	11.4	76.0	74	12	BF528890	BF528890 602043353
	39	11.4	76.0	77	9	AA387938	AA387938 vc87h07.r
	40	11.4	76.0	77	14	T62949	T62949 yb99h02.s1
	41	11.4	76.0	85	9	AI167298	AI167298 ox65c07.s
	42	11.4	76.0	85	9	AA469098	AA469098 ne16g10.s
	43	11.4	76.0	85	9	AA529090	AA529090 vi32d12.r
	44	11.4	76.0	90	9	AA213781	AA213781 zr92g11.r
	45	11.4	76.0	91	9	AA089130	AA089130 mo21a01.r

ALIGNMENTS

RESULT 1
BM023447/c
LOCUS BM023447 75 bp mRNA linear EST 12-MAR-2002
DEFINITION ie80e10.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5673307 5', mRNA sequence.
ACCESSION BM023447
VERSION BM023447.1 GI:16537803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 75)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T. , Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other_ESTs: ie80e10.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

```
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Douglas Melton DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Juliana Brown
            (brown@fas.harvard.edu)
            Putative full length read
            vector to vector length is 76 This sequence now available from the
            IMAGE consortium, for clone orders contact: info@image.llnl.gov.
FEATURES              Location/Qualifiers
     source           1. .75
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5673307"
                      /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
                      /sex="Both"
                      /tissue_type="Islets of Langerhans"
                      /dev_stage="Adult"
                      /lab_host="DH10B"
                      /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
                      Site_2: Sal 1; Starting library constructed using
                      SuperScript Plasmid Library kit (Life Technologies). cDNA
                      made by oligo-dT priming. Size-selected by column
                      fractionation; average insert size 1.08 kb. Library was
                      amplified once on solid support and plasmid DNA from
                      library was prepared. The library DNA was normalized by
                      method #4 from Bonaldo, Lennon, and Soares 1996 Genome
                      Research 6:791-806; 0.5 microgram single-stranded library
                      plasmid DNA was mixed with 5 micrograms PCR product
                      representing library inserts and hybridized to an Ecot of
                      20. Single-stranded (unhybridized) plasmids were isolated
                      by hydroxyapatite chromatography and used to make this
                      library."
BASE COUNT       23 a     25 c     12 g     15 t
ORIGIN

  Query Match             89.3%;  Score 13.4;  DB 13;  Length 75;
  Best Local Similarity   93.3%;  Pred. No. 6.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCACT 15
           | ||||||||||||||
Db      50 TACATGGTGCTCACT 36


RESULT 2
AI022662
LOCUS       AI022662                 58 bp    mRNA    linear   EST 18-JUN-1998
DEFINITION  ox05h11.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1655493 3' similar to SW:TCX1_HUMAN Q15763 T-COMPLEX
            TESTIS-SPECIFIC PROTEIN 1 HOMOLOG ;, mRNA sequence.
ACCESSION   AI022662
VERSION     AI022662.1  GI:3237903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .58
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1655493"
                      /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                      /sex="male"
                      /dev_stage="20 week-post conception fetus"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                      with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                      This is a subtracted version of the original Soares fetal
                      liver spleen 1NFLS library.  1st strand cDNA was primed
                      with a Pac I - oligo(dT) primer [5'
                      AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Pac I and cloned into the Pac I
                      and Eco RI sites of the modified pT7T3 vector.  Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT       14 a     18 c      8 g     17 t      1 others
ORIGIN

  Query Match             82.7%;  Score 12.4;  DB 9;  Length 58;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCACT 15
           | ||||||||||||
Db      37 CAATGGTGCTCACT 50


RESULT 3
AL362924
LOCUS       AL362924                 74 bp    mRNA    linear   EST 04-AUG-2000
DEFINITION  AL362924 ICRFp 522 and 523 Mus musculus cDNA clone K9303B05 5',
            mRNA sequence.
ACCESSION   AL362924
VERSION     AL362924.1  GI:9692322
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Eickhoff,H., Schuchhardt,J., Ivanov,I., Meier-Ewert,S., O'Brien,J.,
            Malik,A., Tandon,N., Wolski,E., Rohlfs,E., Nyarsik,L., Reinhardt,R.
            , Nietfeld,W. and Lehrach,H.
  TITLE     Tissue gene expression analysis using arrayed normalized cDNA
            libraries
  JOURNAL   Genome Res.,  (2000) In press
COMMENT     Contact: MPIMG
            Abt.Lehrach
            Max Planck Institut Fuer Molekulare Genetik
            Ihnestrasse 73, Berlin, 14195 Germany
            The cDNA libraries ICRFp 522 and 523 were normalized with
            oligonucleotide fingerprinting, resulting in a unique subset of
            5376 cDNA clones.
FEATURES              Location/Qualifiers
     source           1. .74
                      /organism="Mus musculus"
                      /strain="C57BL/6"
                      /db_xref="taxon:10090"
                      /clone="K9303B05"
                      /clone_lib="ICRFp 522 and 523"
                      /tissue_type="embryo"
                      /dev_stage="9 and 12 pc embryo"
                      /note="Vector: pGEM T-easy; cDNA subtraction library
                      specific for invasive trophoblast cloned into the pGEM
                      T-easy vector (Promega)"
BASE COUNT       22 a     14 c     26 g     12 t
ORIGIN

  Query Match             82.7%;  Score 12.4;  DB 9;  Length 74;
  Best Local Similarity   92.9%;  Pred. No. 2e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy      2 CCATGGTGCTCACT 15
          ||||||||||| ||
Db      8 CCATGGTGCTCTCT 21


RESULT 4
W15664
LOCUS       W15664                    77 bp    mRNA    linear   EST 10-SEP-1996
DEFINITION  mb52d02.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:333027 5' similar to gb:V00714 Mouse gene for alpha-globin
            (MOUSE);, mRNA sequence.
ACCESSION   W15664
VERSION     W15664.1  GI:1290047
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 77)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:214427
            Seq primer: ETPrimer
            High quality sequence stop: 70.
FEATURES             Location/Qualifiers
     source          1. .77
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:333027"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
BASE COUNT       23 a     15 c     28 g     11 t
ORIGIN

  Query Match             82.7%;  Score 12.4;  DB 14;  Length 77;
  Best Local Similarity   92.9%;  Pred. No. 2.1e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCATGGTGCTCACT 15
          ||||||||||| ||
Db     18 CCATGGTGCTCTCT 31


RESULT 5
AV832470/c
LOCUS       AV832470                  80 bp    mRNA    linear   EST 22-JUN-2001
DEFINITION  AV832470 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
            vulgare leaves vegetative stage Hordeum vulgare subsp. vulgare cDNA
            clone baak3f24, mRNA sequence.
ACCESSION   AV832470
VERSION     AV832470.1  GI:14524559
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 80)
  AUTHORS   Sato,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kazuhiro Sato
            Research Institute for Bioresources
            Okayama University, Barley Germplasm Center
            Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
            Email: kazsato@rib.okayama-u.ac.jp,
            URL:http://www.rib.okayama-u.ac.jp/barley/
            Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
            submission;
            database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES             Location/Qualifiers
     source          1. .80
                     /organism="Hordeum vulgare subsp. vulgare"
                     /cultivar="Akashinriki"
                     /db_xref="taxon:112509"
                     /clone="baak3f24"
                     /clone_lib="K. Sato unpublished cDNA library: Hordeum
                     vulgare subsp. vulgare leaves vegetative stage"
                     /tissue_type="leaves"
                     /dev_stage="vegetative stage"
BASE COUNT       25 a     13 c     22 g     14 t      6 others
ORIGIN

  Query Match             82.7%;  Score 12.4;  DB 10;  Length 80;
  Best Local Similarity   92.9%;  Pred. No. 2.1e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 CCATGGTGCTCACT 15
          ||||||||||| ||
Db     14 CCATGGTGCTCTCT 1


RESULT 6
BQ566161
LOCUS       BQ566161                  96 bp    mRNA    linear   EST 19-JUN-2002
DEFINITION  gi53e03.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
            clone gi53e03 5', mRNA sequence.
ACCESSION   BQ566161
VERSION     BQ566161.1  GI:21469490
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 96)
  AUTHORS   Kachar,B.
  TITLE     EST analysis of gene expression in the mouse Organ of Corti at the
            onset of hearing
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kachar,B.
            Structural Cell Biology
            National Institute of Deafness and other Communication Disorders
            50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
            Tel: 301-402-1599
            Fax: 301-402-1765
            Email: kacharb@nidcd.nih.gov
            Plate: 53  row: e  column: 03
            Seq primer: M13RPl reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .96
```

/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="gi53e03"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 28 a 19 c 34 g 15 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 14; Length 96;
Best Local Similarity 92.9%; Pred. No. 2.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 CCATGGTGCTCACT 15
           |||||||||||  ||
Db      23 CCATGGTGCTCTCT 36
```

RESULT 7
AZ648327/c
LOCUS AZ648327 62 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0517K13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0517K13 F, DNA sequence.
ACCESSION AZ648327
VERSION AZ648327.1 GI:11780683
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 62)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0517 row: K column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 62.
FEATURES Location/Qualifiers
source 1. .62
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0517K13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 11 a 20 c 15 g 16 t
ORIGIN

Query Match 80.0%; Score 12; DB 17; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2 CCATGGTGCTCA 13
           ||||||||||||
Db      45 CCATGGTGCTCA 34
```

```
RESULT 8
TA138D06P
LOCUS       TA138D06P                 82 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 138d06, forward sequence,
            genomic survey sequence.
ACCESSION   AL465857
VERSION     AL465857.1  GI:11835283
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 82)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .82
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="138d06"
BASE COUNT       33 a     13 c     12 g     24 t
ORIGIN

  Query Match             80.0%;  Score 12;  DB 17;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 ATGGTGCTCACT 15
           ||||||||||||
Db      60 ATGGTGCTCACT 71


RESULT 9
AI930840/c
LOCUS       AI930840                  85 bp    mRNA    linear   EST 30-NOV-2001
DEFINITION  sb43a06.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1015-11 5' similar to TR:Q40290 Q40290 CAS15. [2] TR:Q40334 ;,
            mRNA sequence.
ACCESSION   AI930840
VERSION     AI930840.1  GI:5666804
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 85)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand This clone is
            available through: ResGen, Invitrogen Corp. 2130 South Memorial
            Parkway Huntsville, AL 35801 For further information call: (800
            )-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .85
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-11"
                     /clone_lib="Gm-c1015"
                     /tissue_type="Mature flowers, field grown plants"
                     /lab_host="XL10-Gold"
                     /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
                     XhoI; This cDNA library was constructed from mRNA isolated
                     from mature flowers of field grown plants. The cDNA
                     library was prepared using the Stratagene pBluescript II
                     XR cDNA library construction kit. Complementary DNA was
                     synthesized from mRNA using a primer consisting of a poly
                     (dT) sequence with a XhoI restriction site. EcoRI adapters
                     were ligated to the blunt-ended cDNA fragments followed by
                     XhoI digestion. The cDNA fragments were directionally
                     cloned into the EcoRI-XhoI restriction site of the
                     pBluescript vector. The ligated cDNA fragments were
                     transformed into XL10-Gold host cells. This library was
                     constructed by Dr. Randy Shoemaker and Dr. John
                     Erpelding."
BASE COUNT       25 a     15 c     25 g     20 t
ORIGIN

  Query Match             80.0%;  Score 12;  DB 9;  Length 85;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 CATGGTGCTCAC 14
           ||||||||||||
Db      83 CATGGTGCTCAC 72


RESULT 10
AA690354
LOCUS       AA690354                  90 bp    mRNA    linear   EST 16-DEC-1997
DEFINITION  vt31b01.r1 Barstead mouse proximal colon MPLRB6 Mus musculus cDNA
            clone IMAGE:1164649 5', mRNA sequence.
ACCESSION   AA690354
VERSION     AA690354.1  GI:2691290
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
```

WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:630561
Putative full length read
vector to vector length is 147
Seq primer: -28m13 rev2 ET from Amersham.

FEATURES Location/Qualifiers
source 1. .90
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1164649"
/clone_lib="Barstead mouse proximal colon MPLRB6"
/dev_stage="7 day juvenile"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "

BASE COUNT 26 a 26 c 16 g 22 t
ORIGIN

Query Match 80.0%; Score 12; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CATGGTGCTCAC 14
||||||||||||
Db 18 CATGGTGCTCAC 29

RESULT 11
AZ590927/c
LOCUS AZ590927 92 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0400G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0400G16 R, DNA sequence.
ACCESSION AZ590927
VERSION AZ590927.1 GI:11713117
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 92)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0400 row: G column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 92.

FEATURES Location/Qualifiers
source 1. .92
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0400G16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 20 a 24 c 23 g 25 t
ORIGIN

Query Match 80.0%; Score 12; DB 17; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CATGGTGCTCAC 14
||||||||||||
Db 16 CATGGTGCTCAC 5

RESULT 12
TA358F01P/c
LOCUS TA358F01P 38 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 358f01, forward sequence, genomic survey sequence.
ACCESSION AL494114
VERSION AL494114.1 GI:11870743
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available

```
          at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="358f01"
BASE COUNT       16 a      5 c      6 g     11 t
ORIGIN

  Query Match           78.7%;  Score 11.8;  DB 17;  Length 38;
  Best Local Similarity   86.7%;  Pred. No. 2.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCACT 15
           |||||| ||| ||||
Db      30 TCCATGTTGCACACT 16


RESULT 13
AA285022
LOCUS       AA285022                 65 bp    mRNA    linear   EST 15-MAY-1997
DEFINITION  zt25e10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:714186 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS
            (HUMAN);, mRNA sequence.
ACCESSION   AA285022
VERSION     AA285022.1  GI:1927703
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -41m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:714186"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT        7 a     21 c     17 g     20 t
ORIGIN

  Query Match           78.7%;  Score 11.8;  DB 9;  Length 65;
  Best Local Similarity   86.7%;  Pred. No. 3.8e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCACT 15
           |||| ||||||| ||
Db      23 TCCACGGTGCTCCCT 37


RESULT 14
BH805669
LOCUS       BH805669                 70 bp    DNA     linear   GSS 25-APR-2002
DEFINITION  1008061H01.2EL_x1 1008 - RescueMu Grid I Zea mays genomic, DNA
            sequence.
ACCESSION   BH805669
VERSION     BH805669.1  GI:20323197
KEYWORDS    GSS.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1008061  row: 27
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="Zea mays"
                     /cultivar="mixed background W23/A188/B73"
                     /db_xref="taxon:4577"
                     /clone_lib="1008 - RescueMu Grid I"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the  web
                     site www.zmdb.iastate.edu and follow the links for
                     'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
                     extracted from leaf punches,  double digested using BamHI
                     and BglII, and ligated to form circular plasmids.  DH10B
                     cells were transformed and then screened on LB plates with
                     ampicillin."
BASE COUNT        9 a     19 c     11 g     31 t
ORIGIN

  Query Match           78.7%;  Score 11.8;  DB 17;  Length 70;
  Best Local Similarity   86.7%;  Pred. No. 3.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCACT 15
           ||| ||| |||||||
Db      12 TCCCTGGAGCTCACT 26


RESULT 15
AZ799758
LOCUS       AZ799758                 72 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0057G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0057G19 F, DNA sequence.
ACCESSION   AZ799758
VERSION     AZ799758.1  GI:12951196
```

```
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 72)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0057  row: G  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 72.
FEATURES             Location/Qualifiers
     source          1. .72
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0057G19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       13 a     18 c     16 g     25 t
ORIGIN

  Query Match             78.7%;  Score 11.8;  DB 17;  Length 72;
  Best Local Similarity   86.7%;  Pred. No. 4e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCACT 15
           |||||| |||||| |
Db      48 TCCATGTTGCTCATT 62


Search completed: November 21, 2002, 06:51:59
Job time : 2153 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 05:03:29 ; Search time 67 Seconds
(without alignments)
68.659 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	3	US-08-991-830A-3	Sequence 3, Appli
c	2	15	100.0	24	1	US-08-435-350-4	Sequence 4, Appli
	3	14	93.3	15	2	US-08-740-821-1	Sequence 1, Appli
	4	13	86.7	14	4	US-08-666-341A-105	Sequence 105, App
c	5	13	86.7	19	4	US-09-630-155-3	Sequence 3, Appli
	6	13	86.7	20	4	US-09-089-111-3	Sequence 3, Appli
	7	13	86.7	26	4	US-08-463-691-18	Sequence 18, Appl
	8	13	86.7	26	4	US-08-255-236-6	Sequence 6, Appli
c	9	12.4	82.7	22	2	US-08-229-528-5	Sequence 5, Appli
	10	12.4	82.7	47	4	US-09-338-907-248	Sequence 248, App
	11	12.4	82.7	47	4	US-09-218-207-248	Sequence 248, App
c	12	12	80.0	27	1	US-08-503-730-44	Sequence 44, Appl
c	13	12	80.0	53	1	US-08-503-730-29	Sequence 29, Appl
c	14	12	80.0	62	1	US-08-503-730-30	Sequence 30, Appl
	15	11.8	78.7	50	2	US-08-832-468-6	Sequence 6, Appli
c	16	11.8	78.7	54	1	US-08-363-240A-1077	Sequence 1077, Ap
c	17	11.8	78.7	54	4	US-08-584-040-4423	Sequence 4423, Ap
c	18	11.8	78.7	64	1	US-08-290-592E-41	Sequence 41, Appl
c	19	11.8	78.7	64	5	PCT-US96-09448-41	Sequence 41, Appl
	20	11.8	78.7	100	1	US-08-655-086-3	Sequence 3, Appli
	21	11.8	78.7	100	3	US-08-441-971-23	Sequence 23, Appl
	22	11.8	78.7	100	4	US-08-221-653-23	Sequence 23, Appl
	23	11.8	78.7	100	4	US-08-442-144A-23	Sequence 23, Appl
	24	11.8	78.7	100	4	US-08-441-970-23	Sequence 23, Appl
	25	11.4	76.0	15	4	US-09-081-646-198	Sequence 198, App
	26	11.4	76.0	20	3	US-09-280-799-190	Sequence 190, App
	27	11.4	76.0	26	2	US-08-759-581B-16	Sequence 16, Appl
	28	11.4	76.0	26	4	US-09-304-711-16	Sequence 16, Appl
	29	11.4	76.0	26	4	US-09-173-281-16	Sequence 16, Appl
	30	11.4	76.0	30	4	US-09-368-770-8	Sequence 8, Appli
	31	11.4	76.0	30	4	US-09-033-556-15	Sequence 15, Appl
c	32	11.4	76.0	36	4	US-09-198-119C-19	Sequence 19, Appl
c	33	11	73.3	14	5	PCT-US96-05611A-16	Sequence 16, Appl
c	34	11	73.3	15	4	US-08-268-381-1	Sequence 1, Appli
c	35	11	73.3	20	3	US-09-286-904-77	Sequence 77, Appl
c	36	11	73.3	20	4	US-09-640-101-77	Sequence 77, Appl
	37	11	73.3	22	4	US-09-245-248B-63	Sequence 63, Appl
	38	11	73.3	23	4	US-09-177-650-97	Sequence 97, Appl
c	39	11	73.3	27	1	US-08-083-948-9	Sequence 9, Appli
c	40	11	73.3	27	1	US-08-393-785-9	Sequence 9, Appli
c	41	11	73.3	27	1	US-08-475-694-9	Sequence 9, Appli
c	42	11	73.3	27	1	US-08-712-057-9	Sequence 9, Appli
	43	11	73.3	28	3	US-08-441-971-73	Sequence 73, Appl
	44	11	73.3	28	4	US-08-221-653-73	Sequence 73, Appl
	45	11	73.3	28	4	US-08-442-144A-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-08-991-830A-3
; Sequence 3, Application US/08991830A
; Patent No. 6027892
; GENERAL INFORMATION:
; APPLICANT: Chang, Esther H.
; APPLICANT: Pirollo, Kathleen F.
; TITLE OF INVENTION: Compositions and Methods for Reducing Radiation and Drug Re
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sana A. Pratt
; STREET: 10821 Hillbrooke Lane
; CITY: Potomac
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20854
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,830A
; FILING DATE: 16 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/034,160
; FILING DATE: 30 December 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sana A. Pratt
; REGISTRATION NUMBER: 39,441
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 294-9171
; TELEFAX: (301) 294-7357
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
US-08-991-830A-3

Double Pat ??

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGGTGCTCACT 15
|||||||||||||||

```
Db      1 TCCATGGTGCTCACT 15


RESULT 2
US-08-435-350-4/c
; Sequence 4, Application US/08435350
; Patent No. 5599704
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  TREATMENT OF BREAST CANCER
;    NUMBER OF SEQUENCES:  118
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,350
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936,531
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  197/245
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-350-4

  Query Match             100.0%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCACT 15
          |||||||||||||||
Db     21 TCCATGGTGCTCACT 7


RESULT 3
US-08-740-821-1
; Sequence 1, Application US/08740821
; Patent No. 5910583
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, Jeffrey R.
;    APPLICANT:  Vaughn, James P.
;    APPLICANT:  Iglehart, James D.
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson, P.A.
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5910583th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/740,821
;      FILING DATE:  04-NOV-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5405-134
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OLIGONUCLEOTIDE"
US-08-740-821-1

  Query Match             93.3%;  Score 14;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCAC 14
          ||||||||||||||
Db      2 TCCATGGTGCTCAC 15


RESULT 4
US-08-666-341A-105
; Sequence 105, Application US/08666341A
; Patent No. 6365345
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Antisense nucleic Acids for the
;    TITLE OF INVENTION:  prevention and treatment of disorders in which expression
;    TITLE OF INVENTION:  of c-erbB plays a role
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jacobson, Price, Holman and Stern, PLLC
;      STREET:  400 Seventh street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disc
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/666,341A
;      FILING DATE:  15-AUG-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93120710.4
;  INFORMATION FOR SEQ ID NO:  105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  YES
US-08-666-341A-105
```

```
  Query Match             86.7%;  Score 13;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 5
US-09-630-155-3/c
; Sequence 3, Application US/09630155
; Patent No. 6414130
;  GENERAL INFORMATION:
;       APPLICANT: Doherty, Joni Kristin and Gail M. Clinton
;       TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
;       NUMBER OF SEQUENCES: 9
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
;            STREET: 1501 Fourth Avenue, 2600 Century Square
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: U.S.A.
;            ZIP: 98101
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: PC compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/630,155
;            FILING DATE: 16-Jan-2001
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Davison, Barry L.
;            REGISTRATION NUMBER: 47,309
;            REFERENCE/DOCKET NUMBER: 49321-10
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 206 628-7621
;            TELEFAX: 206 628-7699
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 19
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       MOLECULE TYPE: oligonucleotide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-630-155-3

  Query Match             86.7%;  Score 13;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCA 13
          |||||||||||||
Db     13 TCCATGGTGCTCA 1


RESULT 6
US-09-089-111-3
; Sequence 3, Application US/09089111
; Patent No. 6162965
;  GENERAL INFORMATION:
;    APPLICANT:  Hansen, Genevieve
;    TITLE OF INVENTION:  Plant Transformation Methods
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6162965artis Corporation
;      STREET:  3054 Cornwallis Rd.
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/089,111
;      FILING DATE:  02-Jun-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoxie, Thomas
;      REGISTRATION NUMBER:  32,993
;      REFERENCE/DOCKET NUMBER:  CGC1928/R
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8614
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  MTL (P)
US-09-089-111-3

  Query Match             86.7%;  Score 13;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCA 13
          |||||||||||||
Db      6 TCCATGGTGCTCA 18


RESULT 7
US-08-463-691-18
; Sequence 18, Application US/08463691
; Patent No. 6165712
;  GENERAL INFORMATION:
;    APPLICANT:  J. Gordon Foulkes et al.
;    TITLE OF INVENTION:  Methods of Transcriptionally
;    TITLE OF INVENTION:  Modulating Expression of Viral Genes and Genes Useful for t
;    TITLE OF INVENTION:  Production of Proteins
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John P. White, Esq.
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,691
;      FILING DATE:  5-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  26134-G1Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-591-0525
```

```
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-463-691-18

  Query Match             86.7%;  Score 13;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 8
US-08-255-236-6
; Sequence 6, Application US/08255236
; Patent No. 6203976
; GENERAL INFORMATION:
;  APPLICANT:  Foulkes, J. Gordon
;  TITLE OF INVENTION:  METHODS OF TRANSCRIPTIONALLY MODULATING EXPRESSION OF
;  TITLE OF INVENTION:  VIRAL GENES AND GENES USEFUL FOR PRODUCTION OF PROTEINS
;  FILE REFERENCE:  26134g1
;  CURRENT APPLICATION NUMBER: US/08/255,236
;  CURRENT FILING DATE:  1994-06-07
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-255-236-6

  Query Match             86.7%;  Score 13;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 9
US-08-229-528-5/c
; Sequence 5, Application US/08229528
; Patent No. 5837447
;  GENERAL INFORMATION:
;    APPLICANT:  GORSKI, Jack
;    TITLE OF INVENTION:  MONITORING AN IMMUNE RESPONSE BY ANALYSIS OF AMPLIFIED IMMUNO
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  P. O. Box 1497
;      CITY:  Madison
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53701-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette,3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS 3.3
;      SOFTWARE:  WordPerfect, Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/229,528
;      FILING DATE:  18-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,569
;      FILING DATE:  15-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Scanlon, William J.
;      REGISTRATION NUMBER:  30,136
;      REFERENCE/DOCKET NUMBER:  30383/133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 258-4284
;      TELEFAX:  (608) 258-4258
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
US-08-229-528-5

  Query Match             82.7%;  Score 12.4;  DB 2;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 4.3e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCAC 14
          |||| |||||||||
Db     21 TCCAAGGTGCTCAC 8


RESULT 10
US-09-338-907-248
; Sequence 248, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Ilya, Chumakov
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: PROSTATE CANCER GENE
;  FILE REFERENCE: GENSET.18CP1CP
;  CURRENT APPLICATION NUMBER: US/09/338,907
;  CURRENT FILING DATE: 1999-06-23
;  EARLIER APPLICATION NUMBER: 08/996,306
;  EARLIER FILING DATE: 1997-12-22
;  EARLIER APPLICATION NUMBER: 60/099,658
;  EARLIER FILING DATE: 1998-09-09
;  EARLIER APPLICATION NUMBER: 09/218,207
;  EARLIER FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 248
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1..47
;   OTHER INFORMATION: polymorphic fragment 99-148-366
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: polymorphic base G
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..23
;   OTHER INFORMATION: potential microsequencing oligo 99-148-366.mis1
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 25..47
;   OTHER INFORMATION: complement potential microsequencing oligo 99-148-366.mis2
US-09-338-907-248

  Query Match             82.7%;  Score 12.4;  DB 4;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 4.4e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy      1 TCCATGGTGCTCAC 14
          ||| ||||||||||
Db     18 TCCCTGGTGCTCAC 31


RESULT 11
US-09-218-207-248
; Sequence 248, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Ilya, Chumakov
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: Prostate cancer gene
;  FILE REFERENCE: GENSET.018CP1
;  CURRENT APPLICATION NUMBER: US/09/218,207
;  CURRENT FILING DATE: 1998-12-22
;  EARLIER APPLICATION NUMBER: 08/996,306
;  EARLIER FILING DATE: 1997-12-22
;  EARLIER APPLICATION NUMBER: 60/099,658
;  EARLIER FILING DATE: 1998-09-09
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 248
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1..47
;   OTHER INFORMATION: polymorphic fragment 99-148-366
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: polymorphic base G
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..23
;   OTHER INFORMATION: potential microsequencing oligo 99-148-366.mis1
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 25..47
;   OTHER INFORMATION: complement potential microsequencing oligo 99-148-366.mis2
US-09-218-207-248

  Query Match             82.7%;  Score 12.4;  DB 4;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 4.4e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCAC 14
          ||| ||||||||||
Db     18 TCCCTGGTGCTCAC 31


RESULT 12
US-08-503-730-44/c
; Sequence 44, Application US/08503730
; Patent No. 5780269
;  GENERAL INFORMATION:
;    APPLICANT:  Inouye, Sumiko
;    APPLICANT:  Inouye, Masayori
;    TITLE OF INVENTION:  NEW HYBRID MOLECULES
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weiser & Associates
;      STREET:  230 South Fifteenth Street Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/503,730
;      FILING DATE:  18-JUL-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/817,430
;      FILING DATE:  06-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  377(913).6277P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-503-730-44

  Query Match             80.0%;  Score 12;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 CCATGGTGCTCA 13
          ||||||||||||
Db     16 CCATGGTGCTCA 5


RESULT 13
US-08-503-730-29/c
; Sequence 29, Application US/08503730
; Patent No. 5780269
;  GENERAL INFORMATION:
;    APPLICANT:  Inouye, Sumiko
;    APPLICANT:  Inouye, Masayori
;    TITLE OF INVENTION:  NEW HYBRID MOLECULES
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weiser & Associates
;      STREET:  230 South Fifteenth Street Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/503,730
;      FILING DATE:  18-JUL-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/817,430
;      FILING DATE:  06-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  377(913).6277P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
```

```
;      STRANDEDNESS:  single
;      TOPOLOGY:  both
US-08-503-730-29

  Query Match             80.0%;  Score 12;  DB 1;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCA 13
           ||||||||||||
Db      13 CCATGGTGCTCA 2


RESULT 14
US-08-503-730-30/c
; Sequence 30, Application US/08503730
; Patent No. 5780269
;  GENERAL INFORMATION:
;    APPLICANT:  Inouye, Sumiko
;    APPLICANT:  Inouye, Masayori
;    TITLE OF INVENTION:  NEW HYBRID MOLECULES
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weiser & Associates
;      STREET:  230 South Fifteenth Street Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/503,730
;      FILING DATE:  18-JUL-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/817,430
;      FILING DATE:  06-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  377(913).6277P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  both
US-08-503-730-30

  Query Match             80.0%;  Score 12;  DB 1;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCA 13
           ||||||||||||
Db      13 CCATGGTGCTCA 2


RESULT 15
US-08-832-468-6
; Sequence 6, Application US/08832468
; Patent No. 5962237
;  GENERAL INFORMATION:
;    APPLICANT:  Ts'o, Paul O.P.
;    APPLICANT:  Wang, Zheng-Pin
;    APPLICANT:  Lesko, Stephen A.
;    APPLICANT:  Nelson, William G.
;    APPLICANT:  Partin, Alan W.
;    TITLE OF INVENTION:  A METHOD OF ENRICHING RARE CELLS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  700 Thirteenth St., NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,468
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60-014929
;      FILING DATE:  05-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Jeremy M.
;      REGISTRATION NUMBER:  33587
;      REFERENCE/DOCKET NUMBER:  72466
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-737-6770
;      TELEFAX:  202-737-6776
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid (synthetic DNA)
US-08-832-468-6

  Query Match             78.7%;  Score 11.8;  DB 2;  Length 50;
  Best Local Similarity   86.7%;  Pred. No. 9.3e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCACT 15
           ||||| |||||| ||
Db      19 TCCATAGTGCTCCCT 33


Search completed: November 21, 2002, 06:53:17
Job time : 69 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 06:15:59 ; Search time 83 Seconds
(without alignments)
68.445 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 195614

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	12.4	82.7	47	9	US-09-853-526-248	Sequence 248, App
	2	12.4	82.7	47	10	US-09-901-484A-248	Sequence 248, App
c	3	11.8	78.7	64	10	US-09-158-120A-41	Sequence 41, Appl
	4	11.8	78.7	71	10	US-09-783-590-4259	Sequence 4259, Ap
c	5	11.4	76.0	17	10	US-09-866-108-1434	Sequence 1434, Ap
c	6	11.4	76.0	17	10	US-09-866-108-1435	Sequence 1435, Ap
c	7	11.4	76.0	17	10	US-09-866-108-1436	Sequence 1436, Ap
c	8	11.4	76.0	17	10	US-09-866-108-1437	Sequence 1437, Ap
c	9	11.4	76.0	17	10	US-09-866-108-1438	Sequence 1438, Ap
	10	11.4	76.0	17	10	US-09-866-108-6654	Sequence 6654, Ap
	11	11.4	76.0	17	10	US-09-866-108-6655	Sequence 6655, Ap
	12	11.4	76.0	17	10	US-09-866-108-6656	Sequence 6656, Ap
	13	11.4	76.0	17	10	US-09-866-108-6657	Sequence 6657, Ap
	14	11.4	76.0	17	10	US-09-866-108-6658	Sequence 6658, Ap
c	15	11.4	76.0	17	10	US-09-866-108-8318	Sequence 8318, Ap
c	16	11.4	76.0	17	10	US-09-866-108-8319	Sequence 8319, Ap
c	17	11.4	76.0	17	10	US-09-866-108-8320	Sequence 8320, Ap
c	18	11.4	76.0	17	10	US-09-866-108-8321	Sequence 8321, Ap
c	19	11.4	76.0	17	10	US-09-866-108-8322	Sequence 8322, Ap
	20	11.4	76.0	20	10	US-09-800-629A-190	Sequence 190, App
c	21	11.4	76.0	25	10	US-09-866-108-4363	Sequence 4363, Ap
c	22	11.4	76.0	25	10	US-09-866-108-4364	Sequence 4364, Ap
c	23	11.4	76.0	25	10	US-09-866-108-4365	Sequence 4365, Ap
c	24	11.4	76.0	25	10	US-09-866-108-4366	Sequence 4366, Ap
c	25	11.4	76.0	25	10	US-09-866-108-4367	Sequence 4367, Ap
c	26	11.4	76.0	25	10	US-09-866-108-4368	Sequence 4368, Ap
c	27	11.4	76.0	25	10	US-09-866-108-4369	Sequence 4369, Ap
c	28	11.4	76.0	25	10	US-09-866-108-4370	Sequence 4370, Ap
c	29	11.4	76.0	25	10	US-09-866-108-4371	Sequence 4371, Ap
c	30	11.4	76.0	25	10	US-09-866-108-4372	Sequence 4372, Ap
c	31	11.4	76.0	25	10	US-09-866-108-4373	Sequence 4373, Ap
c	32	11.4	76.0	25	10	US-09-866-108-4374	Sequence 4374, Ap
c	33	11.4	76.0	25	10	US-09-866-108-4375	Sequence 4375, Ap
	34	11.4	76.0	25	10	US-09-866-108-11546	Sequence 11546, A
	35	11.4	76.0	25	10	US-09-866-108-11547	Sequence 11547, A
	36	11.4	76.0	25	10	US-09-866-108-11548	Sequence 11548, A
	37	11.4	76.0	25	10	US-09-866-108-11549	Sequence 11549, A
	38	11.4	76.0	25	10	US-09-866-108-11550	Sequence 11550, A
	39	11.4	76.0	25	10	US-09-866-108-11551	Sequence 11551, A
	40	11.4	76.0	25	10	US-09-866-108-11552	Sequence 11552, A
	41	11.4	76.0	25	10	US-09-866-108-11553	Sequence 11553, A
	42	11.4	76.0	25	10	US-09-866-108-11554	Sequence 11554, A
	43	11.4	76.0	25	10	US-09-866-108-11555	Sequence 11555, A
	44	11.4	76.0	25	10	US-09-866-108-11556	Sequence 11556, A
	45	11.4	76.0	25	10	US-09-866-108-11557	Sequence 11557, A

ALIGNMENTS

RESULT 1
US-09-853-526-248
; Sequence 248, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 248
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; OTHER INFORMATION: polymorphic fragment 99-148-366
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: polymorphic base G
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 99-148-366.mis1
; NAME/KEY: primer_bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 99-148-366.mis2
US-09-853-526-248

```
  Query Match             82.7%;  Score 12.4;  DB 9;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 5.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCAC 14
          ||| ||||||||||
Db     18 TCCCTGGTGCTCAC 31


RESULT 2
US-09-901-484A-248
; Sequence 248, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: Prostate Cancer Gene
;  FILE REFERENCE: GEN-T111XC3D2
;  CURRENT APPLICATION NUMBER: US/09/901,484A
;  CURRENT FILING DATE:  2001-07-09
;  PRIOR APPLICATION NUMBER: US 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: US 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: US 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: US 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: US 09/853,526
;  PRIOR FILING DATE: 2001-05-11
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: (1)..(47)
;   OTHER INFORMATION: polymorphic fragment 99-148-366
;   NAME/KEY: allele
;   LOCATION: (24)..(24)
;   OTHER INFORMATION: polymorphic base G
;   NAME/KEY: primer_bind
;   LOCATION: (1)..(23)
;   OTHER INFORMATION: potential microsequencing oligo 99-148-366.mis1
;   NAME/KEY: primer_bind
;   LOCATION: (25)..(47)
;   OTHER INFORMATION: complement potential microsequencing oligo 99-148-366.mis2
US-09-901-484A-248

  Query Match             82.7%;  Score 12.4;  DB 10;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 5.1e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCAC 14
          ||| ||||||||||
Db     18 TCCCTGGTGCTCAC 31


RESULT 3
US-09-158-120A-41/c
; Sequence 41, Application US/09158120A
; Patent No. US20020102257A1
;  GENERAL INFORMATION:
;    APPLICANT:  JOHNSON, L.
;    TITLE OF INVENTION:  Human Murine Chimeric Antibodies Against
;    TITLE OF INVENTION:  Respiratory Syncytical Virus
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;      ADDRESSEE:  STEWART &  OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  P160
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  MS Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/158,120A
;      FILING DATE:  September 21, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/290,592
;      FILING DATE:  August 15, 1994
;      APPLICATION NUMBER:  07/813,372
;      FILING DATE:  December 23, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  469201-367
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  973-994-1700
;      TELEFAX:  973-994-1744
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  64 NUCLEOTIDES
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-09-158-120A-41

  Query Match             78.7%;  Score 11.8;  DB 10;  Length 64;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCACT 15
          |||||| || |||||
Db     24 TCCATGTTGGTCACT 10


RESULT 4
US-09-783-590-4259
; Sequence 4259, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Patrick J.
;  APPLICANT:  Haseltine, William A.
;  APPLICANT:  Li, Haodong
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
;  FILE REFERENCE: PO-16.2C1
;  CURRENT APPLICATION NUMBER: US/09/783,590
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 08/420,856
;  PRIOR FILING DATE: 1995-04-12
;  PRIOR APPLICATION NUMBER: 08/346,731
;  PRIOR FILING DATE: 1994-11-21
;  NUMBER OF SEQ ID NOS: 12485
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4259
;   LENGTH: 71
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (6)
;   OTHER INFORMATION: n equals a,t,g, or c
```

```
;   NAME/KEY: misc feature
;   LOCATION: (31)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (44)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (58)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (65)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-4259

  Query Match             78.7%;  Score 11.8;  DB 10;  Length 71;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCACT 15
           ||||||||||  ||
Db      16 TCCATGGTGCTGCCT 30


RESULT 5
US-09-866-108-1434/c
; Sequence 1434, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1434
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-1434

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCAC 14
           |||| ||||||||
Db      17 CCATTGTGCTCAC 5


RESULT 6
US-09-866-108-1435/c
; Sequence 1435, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1435
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-1435

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCAC 14
           |||| ||||||||
```

```
Db      16 CCATTGTGCTCAC 4


RESULT 7
US-09-866-108-1436/c
; Sequence 1436, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1436
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-1436

  Query Match            76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity  92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCAC 14
           |||| ||||||||
Db      15 CCATTGTGCTCAC 3


RESULT 8
US-09-866-108-1437/c
; Sequence 1437, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1437
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-1437

  Query Match            76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity  92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCAC 14
           |||| ||||||||
Db      14 CCATTGTGCTCAC 2


RESULT 9
US-09-866-108-1438/c
; Sequence 1438, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
```

```
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1438
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-1438

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 CCATGGTGCTCAC 14
           |||| ||||||||
Db      13 CCATTGTGCTCAC 1


RESULT 10
US-09-866-108-6654
; Sequence 6654, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6654
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-6654

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 CATGGTGCTCACT 15
           ||||| |||||||
Db       5 CATGGGGCTCACT 17


RESULT 11
US-09-866-108-6655
; Sequence 6655, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
```

```
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6655
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-6655

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 CATGGTGCTCACT 15
           ||||| |||||||
Db       4 CATGGGGCTCACT 16


RESULT 12
US-09-866-108-6656
; Sequence 6656, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6656
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-6656

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 CATGGTGCTCACT 15
           ||||| |||||||
Db       3 CATGGGGCTCACT 15


RESULT 13
US-09-866-108-6657
; Sequence 6657, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6657
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-6657

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       3 CATGGTGCTCACT 15
           ||||| |||||||
Db       2 CATGGGGCTCACT 14


RESULT 14
US-09-866-108-6658
; Sequence 6658, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6658
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-6658

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 CATGGTGCTCACT 15
           ||||| |||||||
Db       1 CATGGGGCTCACT 13


RESULT 15
US-09-866-108-8318/c
; Sequence 8318, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8318
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-8318

  Query Match             76.0%;  Score 11.4;  DB 10;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCA 13
           |||||||||| ||
Db      17 TCCATGGTGCCCA 5


Search completed: November 21, 2002, 07:59:02
Job time : 83 secs
```

Priority Date: 12/20/96

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 03:45:54 ; Search time 3161 Seconds
(without alignments)
138.103 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15	100.0	19	6	AX103821	AX103821 Sequence
2		15	100.0	19	6	AX355038	AX355038 Sequence
3	c	15	100.0	24	6	I34918	I34918 Sequence 4
4		14	93.3	15	6	AR071406	AR071406 Sequence
5		14	93.3	51	6	AX159179	AX159179 Sequence
6		13	86.7	14	6	A45228	A45228 Sequence 10
7		13	86.7	14	6	A88989	A88989 Sequence 11
8		13	86.7	14	6	AR202871	AR202871 Sequence
9		13	86.7	16	6	A88177	A88177 Sequence 32
10		13	86.7	16	6	A90144	A90144 Sequence 32
11		13	86.7	20	6	AR137074	AR137074 Sequence
12	c	13	86.7	20	6	AX164704	AX164704 Sequence
13		13	86.7	26	6	AR122156	AR122156 Sequence
14		13	86.7	26	6	AR142598	AR142598 Sequence
15	c	12.4	82.7	22	6	AR054584	AR054584 Sequence
16	c	12.4	82.7	24	6	AX428032	AX428032 Sequence
17	c	12.4	82.7	50	6	AX161043	AX161043 Sequence
18		12.4	82.7	51	6	AX159180	AX159180 Sequence
19	c	12.4	82.7	51	6	AX161039	AX161039 Sequence
20	c	12.4	82.7	51	6	AX161040	AX161040 Sequence
21	c	12.4	82.7	51	6	AX161041	AX161041 Sequence
22		12.4	82.7	98	6	AX385593	AX385593 Sequence
23	c	12	80.0	22	6	E15265	E15265 Primer. 7/1
24	c	12	80.0	27	6	AR017897	AR017897 Sequence
25	c	12	80.0	53	6	AR017882	AR017882 Sequence
26	c	12	80.0	62	6	AR017883	AR017883 Sequence
27		12	80.0	97	6	E15263	E15263 Chlamydomon
28	c	11.8	78.7	19	6	AX375647	AX375647 Sequence
29		11.8	78.7	50	6	AR077265	AR077265 Sequence
30		11.8	78.7	50	6	AX199506	AX199506 Sequence
31		11.8	78.7	51	6	AX199505	AX199505 Sequence
32	c	11.8	78.7	54	6	AR188935	AR188935 Sequence
33	c	11.8	78.7	64	6	AR048884	AR048884 Sequence
34		11.8	78.7	72	9	AF159095	AF159095 Homo sapi
35		11.8	78.7	76	6	AX389427	AX389427 Sequence
36	c	11.8	78.7	93	9	AF172205	AF172205 Nycticebu
37	c	11.8	78.7	93	9	AF172208	AF172208 Eulemur m
38	c	11.8	78.7	93	9	AF172209	AF172209 Perodicti
39		11.8	78.7	96	3	CELE11937	AJ011937 Caenorhab
40		11.8	78.7	100	6	AR048314	AR048314 Sequence
41		11.8	78.7	100	6	AR097085	AR097085 Sequence
42		11.8	78.7	100	6	AR130583	AR130583 Sequence
43		11.8	78.7	100	6	AR171932	AR171932 Sequence
44		11.4	76.0	15	6	AR180130	AR180130 Sequence
45		11.4	76.0	20	6	AR136387	AR136387 Sequence

ALIGNMENTS

RESULT 1
AX103821
LOCUS AX103821 19 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 13 from Patent WO0122972.
ACCESSION AX103821
VERSION AX103821.1 GI:13920018
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 13-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

```
          GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        3 a      6 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCACT 15
          |||||||||||||||
Db      4 TCCATGGTGCTCACT 18


RESULT 2
AX355038
LOCUS       AX355038                 19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 66 from Patent WO0197843.
ACCESSION   AX355038
VERSION     AX355038.1  GI:18619705
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 66 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"
BASE COUNT        3 a      6 c      5 g      5 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCACT 15
          |||||||||||||||
Db      4 TCCATGGTGCTCACT 18


RESULT 3
I34918/c
LOCUS       I34918                   24 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 4 from patent US 5599704.
ACCESSION   I34918
VERSION     I34918.1  GI:2087886
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Thompson,J.D. and Draper,K.G.
  TITLE     ErbB2/neu targeted ribozymes
  JOURNAL   Patent: US 5599704-A 4 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        6 a      7 c      8 g      3 t
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCACT 15
          |||||||||||||||
Db     21 TCCATGGTGCTCACT 7


RESULT 4
AR071406
LOCUS       AR071406                 15 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 1 from patent US 5910583.
ACCESSION   AR071406
VERSION     AR071406.1  GI:7222294
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Marks,J.R., Vaughn,J.P. and Inglehart,J.D.
  TITLE     Antisense oligonucleotides against ERBB-2
  JOURNAL   Patent: US 5910583-A 1 08-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        2 a      6 c      3 g      4 t
ORIGIN

  Query Match              93.3%;  Score 14;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCAC 14
          ||||||||||||||
Db      2 TCCATGGTGCTCAC 15


RESULT 5
AX159179
LOCUS       AX159179                 51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2507 from Patent WO0140521.
ACCESSION   AX159179
VERSION     AX159179.1  GI:14540510
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 2507 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (2508 is other entry)
                     Accession number cg39714236"
BASE COUNT        7 a      14 c     15 g     15 t
ORIGIN

  Query Match              93.3%;  Score 14;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 CCATGGTGCTCACT 15
          ||||||||||||||
Db     17 CCATGGTGCTCACT 30


RESULT 6
```

```
A45228
LOCUS       A45228                    14 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 105 from Patent WO9517507.
ACCESSION   A45228
VERSION     A45228.1  GI:2299723
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W., Schlingensiepen,K., Schlingensiepen,R. and
            Schlingensiepen,G.
  TITLE     ANTISENSE NUCLEIC ACIDS FOR THE PREVENTION AND TREATMENT OF
            DISORDERS IN WHICH EXPRESSION OF c-erbB PLAYS A ROLE
  JOURNAL   Patent: WO 9517507-A 105 29-JUN-1995;
            BIOGNOSTIK GES (DE)
COMMENT     Other publication AU 1313095 950710.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c      4 g      4 t
ORIGIN

  Query Match           86.7%;  Score 13;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 7
A88989
LOCUS       A88989                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1137 from Patent WO9833904.
ACCESSION   A88989
VERSION     A88989.1  GI:6737559
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 1137 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c      4 g      4 t
ORIGIN

  Query Match           86.7%;  Score 13;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 8
AR202871
LOCUS       AR202871                  14 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 105 from patent US 6365345.
ACCESSION   AR202871
VERSION     AR202871.1  GI:21499111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W., Schlingensiepen,K.-H., Schlingensiepen,R. and
            Schlingensiepen,G.-F.
  TITLE     Antisense nucleic acids for the prevention and treatment of
            disorders in which expression of c-erbB plays a role
  JOURNAL   Patent: US 6365345-A 105 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
BASE COUNT        2 a      4 c      4 g      4 t
ORIGIN

  Query Match           86.7%;  Score 13;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 9
A88177
LOCUS       A88177                    16 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 325 from Patent WO9833904.
ACCESSION   A88177
VERSION     A88177.1  GI:6736747
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 325 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      5 c      5 g      4 t
ORIGIN

  Query Match           86.7%;  Score 13;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 10
A90144
LOCUS       A90144                    16 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 325 from Patent EP0856579.
ACCESSION   A90144
VERSION     A90144.1  GI:6738658
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 325 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      5 c      5 g      4 t
```

```
ORIGIN

  Query Match             86.7%;  Score 13;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 11
AR137074
LOCUS       AR137074                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 3 from patent US 6162965.
ACCESSION   AR137074
VERSION     AR137074.1  GI:14478324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hansen,G.
  TITLE     Plant transformation methods
  JOURNAL   Patent: US 6162965-A 3 19-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      4 c      7 g      5 t
ORIGIN

  Query Match             86.7%;  Score 13;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TCCATGGTGCTCA 13
          |||||||||||||
Db      6 TCCATGGTGCTCA 18


RESULT 12
AX164704/c
LOCUS       AX164704                  20 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 9 from Patent WO0136644.
ACCESSION   AX164704
VERSION     AX164704.1  GI:14545596
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Rastelli,L., Lewin,D., Taillon,B. and Andrew,D.P.
  TITLE     Wnt-regulated cytokine-like polypeptide and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0136644-A 9 25-MAY-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        7 a      6 c      5 g      2 t
ORIGIN

  Query Match             86.7%;  Score 13;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db     20 CATGGTGCTCACT 8


RESULT 13
AR122156
LOCUS       AR122156                  26 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 18 from patent US 6165712.
ACCESSION   AR122156
VERSION     AR122156.1  GI:14106473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Foulkes,J.Gordon., Leichtfried,F.E., Pieler,C., Stephenson,J.R. and
            Case,C.C.
  TITLE     Methods of transcriptionally modulating expression of viral genes
            and genes useful for production of proteins
  JOURNAL   Patent: US 6165712-A 18 26-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        2 a      11 c      8 g      5 t
ORIGIN

  Query Match             86.7%;  Score 13;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 14
AR142598
LOCUS       AR142598                  26 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6203976.
ACCESSION   AR142598
VERSION     AR142598.1  GI:15103884
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Foulkes,J.Gordon., Leichtfried,F.E., Pieler,C. and Stephenson,J.R.
  TITLE     Methods of preparing compositions comprising chemicals capable of
            transcriptional modulation
  JOURNAL   Patent: US 6203976-A 6 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        2 a      11 c      8 g      5 t
ORIGIN

  Query Match             86.7%;  Score 13;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 CATGGTGCTCACT 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT 15
AR054584/c
LOCUS       AR054584                  22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5837447.
ACCESSION   AR054584
VERSION     AR054584.1  GI:5980161
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Gorski,J.
```

```
  TITLE     Monitoring an immune response by analysis of amplified
            immunoglobulin or T-cell-receptor nucleic acid
  JOURNAL   Patent: US 5837447-A 5 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT        6 a      3 c      8 g      5 t
ORIGIN

  Query Match             82.7%;  Score 12.4;  DB 6;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 8.2e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TCCATGGTGCTCAC 14
           |||| |||||||||
Db      21 TCCAAGGTGCTCAC 8


Search completed: November 21, 2002, 06:15:54
Job time : 3163 secs
```

6,203,976
6,165,712
6,162,965
6,365,345
WO 95/17507 A
5,910,583 (obt by one base)
5,599,704
D.P.
6,027,892
only one with bases 1-15
WO 9323057 ??